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 > o ^
 o | o  IntelliGenetics
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GENALIGN - Multiple Sequence Alignment Program
Release 5.4

Wed 26 Nov 103 6:55:28-PST

Solution Parameters:

```
Nucleic Alphabet    = Identity
Output line length  = 80
Compress            = Off
Histogram           = Off
Randomization       = Off
```

AMINO-Res-length   = 2
Deletion-weight   = 5.00
Length-factor   = 0
Matching-weight   = 1.00
NUCLEIC-Res-length   = 4
Spread-factor   = 50

Clustered order of selected sequences:

```
21.  US-09-835-992A-21    (1-994)
22.  US-09-835-992A-22    (1-843)
19.  US-09-835-992A-19    (1-714)
20.  US-09-835-992A-20    (1-687)
```

Region Alignment: (listed in Clustered order)

```
US-09-835-     1   ctcaccagttgctcctcagatgttcgggtatgctgctggaaagaagaacatatggaaaaatatgg
consensus          ctcaccagttgctcctcagatgttcgggtatgctgctggaaagaagaacatatggaaaaatatgg

US-09-835-     1   cgtattcccagtccaagatgaatacagttcAgaTgaagtgcAtctaAAgaagttT
US-09-835-     1   AAnTTATTTnAATTTCCTATTTAAnCnTcCT
US-09-835-     1   AAgTTTATTTTTAATTTTCTTATTTAAACATTCT
consensus          ATTTTAATTTTTCTTATTTAAACATTCT

US-09-835-    62   aacaaaaattgaacacttgCAAAAAAttggatggaaaaaatcataaacattcagttaataac
US-09-835-     1   gGCCAAAAA
US-09-835-     1   cGCCAgAAA
consensus          ctcaccagttgctcctcagatgttcgggtatgctgctggaaagaagaacatatggaaaaatatgg
```

US-09-835-   26   TCTCAAAGCATTATTTTTATCCTATATCTCACTGAATTTTAAnAAAATAACATTAGTATTAGA
consensus   tcttcaaagcattaTTtTtatCCtATAtctcaCtgaaTttTAAgaaataacaCattagtatTga

US-09-835-   245   ggCCagtGaAgcActtcgTTACagaagtgATggccctgCaaTccaaagctgtGGAAnTTTtggCa
US-09-835-   101   AAAACCTTnGGAAAAAAAAnAGTAAAATAAnTAATTAAACCTTnCrTGAAAAAnGGAAnTTTnTACC
US-09-835-   101   AAAAACTAGGAAAAAAAGAGTAAAATGCAGATAATTAAAACTTATTAAAAAATGAAAATTATAAC
US-09-835-   87   AAAAACTAGGAAAAAAnAGATnnAATGCAGATAATTAAACTTACATGAAAAAAGGAAAATATAAC
consensus   aaa-ctaGgAaaAaagaTaaatgcagATaattaa-ctTaCatgaaaaaGGAAA-TTtata-c

US-09-835-   306   cAaGaAntgADAtgacCtgacTtgccaagctcgtcgtttgaAgaAaaaaagcAttattaaaatggtcg
US-09-835-   162   AAnGGACnGAAAnCnTnTAAcTTngGAAnTnnAATTATAnTTAnGAAAnCggCnnCnGAAAAcc
US-09-835-   162   AAAGGACTGAGAAnCGTTATTAAAATAAGATATTAAnTTTGAAAAATCGAnTTCCAATTTTCCA
US-09-835-   148   AAAGGACTGAGAACGTTATAAAATGAGAGATTATAATTGAAAATTGCAnTCTGAAAAGC
consensus   aAaGgActGAGaaCgttaTaaatgagagaTtAtAattgaaaActgcatctcgaagc

US-09-835-   367   gcttTgatatGagtcAAAgAaggCTgcAaGAaaatgcTatgagAaaatcTggCCTgGACAccaaA
US-09-835-   223   AAnCTTnATgGTtCcAATTATCCTnAAnGAgGGnnTTTnAnnACTAAnTAnCCCnGATTTTCCA
consensus   aaacTttattGgtcaAttat-CTtaAtGATggtgttCtatgAcTaaTac-CtGATttcCA

US-09-835-   428   tgAtattgaaCgtaatagaAACttcacgaTTgcTTtCtccAACgaacTccttaCttatgaA
US-09-835-   284   AtAnGGAAnCnCCCnnnTTAAAAAnTnTTTnnTTnATTTTAAAAAATAACCCnGTnCcAACCCnGA
US-09-835-   284   AgAAGGAAAAnCCCAATTGTTAAAAAATAATTATTTnATTAAAAAAAATAAGCTCTCGA
consensus   AAAACTTTATTGTTCAATTAAAATTAATGATGGTGTTTTATGACTAATACACATTTTTCA

US-09-835-   270   AtAAGGAAAAAACCCATGTTAAAAAAATATTTTTAATTTTTTAnTTTTTAAAAAAATAAGCCTTGTTCAAGCTCTGA
consensus   a-AaggaaaCCcatgtcAAaaatattttCtatTTTaaaAatAA-cctgTgttcAagctccgA

US-09-835-   489   gCActgggacTctgTCcagGAagGacaAGgtgcAacgctggttgattagaggaGAtaatacAt
US-09-835-   345   TCAnATTcCTTnATTTgDATTGGGGAAAAAAATAncngttccnnataccnnGAnnngcaAA
US-09-835-   345   AgAAGGAAAAnCCCAATTGTTAAAAAATAATTATTTnATTAAAAAAAATAAGCTCTCGA
US-09-835-   331   TCAtAtTTCTTTTTnATTTTTTGATTTCGGGAAnAAAAT
consensus   tCAtattcctTcTaTcttttgDatt-gggAagaaaAt-----actgttctgGAtagcat-a

US-09-835-   550   aTggaggAAAagTgggtcataaaTccTagTgggtggacdgattcAaaggGcaccCACTcAGg
US-09-835-   406   nTTttaAATTTTTTAaCCccccCTAnTTnTt TaaAAncTatngAAaAnTnGATnAngACTTGA
US-09-835-   398   AATGCAAAATTTTTAATTTTTTTTAGATTTTTTAATCTCnCTAATTTAAATCTATTTGAGAAATTGATTAA
US-09-835-   384   AATGCAAAAATTTTTAGATTTTTTAATCTCnCTAATTTAAATTACTATTTGAGAAATTGATTAA
consensus   a-tgcaaAActtttag-tttt-at-tcctcaattttaagaac-attGagaaAtt--Tt-a

US-09-835-   611   cgctacCaggtcCttgcTcagtGtcgcagaactctgcTgGcagctgagAgggaagCCggaaAa
consensus || || || |
```

Clustered / continued sequences:

```
US-09-835-   184   tgattctttgacTaTcttacCaAtgttgtcgtccCcacttcagAntgctgcgcagcagcaaTttt
US-09-835-    40   ccnCAAAAnCATTATTTnAcCCTTATTnnAnaAAnTACTcTTnnTTnnTTTnAAA
US-09-835-    40   cgtattcccagtccaagatgaatacagttaagtactatttcaATtt-cTATtAAacattcT
consensus              cgtattcccagtccaagagtgaatacagttaagtactatttcaATtt-cTaTtAAacattcT

US-09-835-    10   aacaaaaattgaacact-gccaaaaatcataaacattcagttaataac
consensus              aacaaaaattgaacact-gccaaaaatcataaacattcagttaataac

US-09-835-   123   ccgtattcccagtccaagatgaatacagttcAgaTgaagtgcAtctaAAgaagttT
US-09-835-    10   AAnTTATTTnAATTTCCTATTTAAnCnTcCT
consensus              tCAtattcttcTaTcttttgDatt-999Aagaaaat-------actgttctgGAtagcat-a

US-09-835-    40   TCTcAAAGCATTATTTTTATCCTATATCTCACTGAnTTTTAAnAAAATAACATTAGTATTAGA
```

```
Alignment score = -2355.00

Scoring matrix:

          19    20    21    22

19
20       524  -1381  -296
21             -1522  -333
22                    -741
```

```
US-09-835-  467  attgcCAacCTantTnCngGccaccngtGgggcnTnGgTnttccTTacTTantcCCCcAAg
US-09-835-  459  TGACATGAAGTGCACAACACTAATTACTCTGGCCAGCTCGTTGGCAATTGTTGTTTCTTACTTAGT
                      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-835-  445  TGACATGAAGTGCACAACACTAATTACTCTGGCCAGCTCGTTGGCAATTGTTGTTTCTTACTTAGT
consensus        tgaca--aag--cac-acac-aattactggccag-tGttggcatt-tgttct--ctta-t

US-09-835-  672  GAggcaaagTtcctgGtgcaaaggtggctcTgcngCaTAAtTtangncattggAggAActgt
US-09-835-  528  GAaanncctTaAnncnGaanctccnccAAaaTaaccttTAAnTATCCTTggtaAccAAanca
                  |||||||| |||| |||||||||||||||||||
US-09-835-  520  TCTCCCAAGGGAAAACTCTTAAaTTGAATCTTCAGCaGaATAATCCTT
                  ||||||||||||||||||||||||||||||||||||||||||||||||
US-09-835-  506  TCTCCCAAGG  AAAACTCTTAAAcTGaATCTTCaGCnGAATAA  CCTT
consensus        aaataTacttgtcagcaaAacaaa-gctctttt-t-tac--agttctt--gattc-ct

US-09-835-  733  ggttgTaacactcTacaagAAtggGggTtttcccggAaGccgCCagttccTCtttagaactCat
US-09-835-  589  AAAccTtTtTTngTTtacntanTccctTGgggaTTTaAcGggtCCccaatTTnaTcngaaCCc
                  |||||||||||||||||||||||||||||||||||||||||
US-09-835-  568  AAATATaACTTtTGTaAGGcaCAaAAAACTTTTTTTTTGTTTTACATAGTTCTTTgGGATTTTACT
                  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
US-09-835-  552  AAATATAACTTtTGTcAGCCAAAACAAAA  CTTTTTGTTTTACATAGTTCTTT GGATTTTACT
consensus        --tccpaag--aaaa-tcttaaa-tgaatcTtcagcA-AAt-atcctt----a;-aa----

US-09-835-  611  GTTCCTAATTTTATTCTGAAAACTCCATTTTTtCC
                  |||||||||||||||||||||||||||||||
US-09-835-  629  GTTCCTAATTTTATTCTGAAATCTCaATTTTACC
consensus        gttccTaatttTattctgaaactc-atTtaCca-t-g--a-n-----c-n---

US-09-835-  650  anTttTccccnAacCatAnttaccCATTTTACC
                  |||||||||||||||||||||||||
US-09-835-  710  cgcAAanceaGtantntccccngncncttccccgANcctgggAAaAAcgGgATTnggTc

US-09-835-  794  caaaaTtgaagcngttccaaccaagctCTgCaagTnaTnghttaAngNaaaatCttNgtt
US-09-835-  855  ttaAAggngGattgagaaggaaacntnaaagaggggaacAANttctgAAagagaaaa
consensus        gttccTaatttTattctgaaactc-atTtaCca-t-g--a-n-----c-n---

US-09-835-  916  atnCggngggAnAtttttgCCccttCaagggggaaanaatgGGccTggggggtaaaagAnggcc
US-09-835-  771  CCcCCccTTAAAAaacaacCttccCCCcnncTTTCgcccaGgnnTTNNTtcccgtCCtaAatccg
                        ||||||         ||||
US-09-835-  676  CC  ataTTAA                    CTTTTG
                  ||                             |||||
US-09-835-  658  CCctatTTAA                     CTTTTG         TTNNT
consensus        cccc--ttaaaa------c------c---cttg----g---Ttnt--gcacag-tgt--

US-09-835-  977  AcCCtggggtgGtgggat
                  ||||
US-09-835-  832  AaCAATaaAaaG
US-09-835-  706  gcCAATtcA
US-09-835-  688
consensus        accaat--a--gtgggat
```